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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,002

DATE: 09/18/2001
TIME: 15:51:22

Input Set : A:\78973-1C seq 28-08-01 v1.txt
Output Set: N:\CRF3\09182001\I943002.raw

3 <110> APPLICANT: Duncan, Roy
5 <120> TITLE OF INVENTION: NOVEL REOVIRUS-DERIVED PROTEINS AND USES THEREFOR
7 <130> FILE REFERENCE: 78973-1C
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/943,002
C--> 10 <141> CURRENT FILING DATE: 2001-08-31
12 <160> NUMBER OF SEQ ID NOS: 15
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1643
18 <212> TYPE: DNA
19 <213> ORGANISM: avian reovirus strain 176
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (25)...(318)
23 <223> OTHER INFORMATION: nucleotide sequence encoding P11 protein (SEQ ID
26 <220> FEATURE:
27 <221> NAME/KEY: misc_feature
28 <222> LOCATION: (293)...(730)
29 <223> OTHER INFORMATION: CDS encoding P16 protein (SEQ ID
30 NO:3)
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <222> LOCATION: (630)...(1607)
35 <223> OTHER INFORMATION: CDS encoding sigma3 protein (SEQ
36 ID NO:4)
38 <400> SEQUENCE: 1
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40 Met Leu Arg Met Pro Pro Gly Ser Cys
41 1 5
43 aac ggt gcg act gct gta ttt ggt aac gtt cat tgt cag gca gct caa 99
44 Asn Gly Ala Thr Ala Val Phe Gly Asn Val His Cys Gln Ala Ala Gln
45 10 15 20 25
47 aac acg gca ggt ggt gat ttg caa gct acg tca tcc ata att gca tat 147
48 Asn Thr Ala Gly Asp Leu Gln Ala Thr Ser Ser Ile Ile Ala Tyr
49 30 35 40
51 tgg cct tat cta gcg gcg ggt ggt ttc tta tta att gtt atc att 195
52 Trp Pro Tyr Leu Ala Ala Gly Gly Phe Leu Leu Ile Val Ile Ile
53 45 50 55
55 ttc gct ctt cta tac tgt tgt aag gct aag gtc aag gcg gac gct gca 243
56 Phe Ala Leu Leu Tyr Cys Cys Lys Ala Lys Val Lys Ala Asp Ala Ala
57 60 65 70
59 cgt agt gtc ttc cat cgt gag ctg gta gcg ttg agt tct ggt aag cac 291
60 Arg Ser Val Phe His Arg Glu Leu Val Ala Leu Ser Ser Gly Lys His
61 75 80 85
63 aat gca atg gct ccg cca tac gac gtt tgaagtgc aa cgatttaatt 338
64 Asn Ala Met Ala Pro Pro Tyr Asp Val
65 90 95
67 tctgtccgct atcacttcgc gaacttgcta tcccatcatt tactgctata actggggctg 398

2.
ENTERED

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68	acccatcaca	gtatttaac	attgagctcc	cacacactca	tcctctctat	tccaaattgc	458
69	ctactctgtt	atctcaacct	tgttagggtcc	acgtgcggct	gattcgccgg	ttcgctctct	518
70	attcaacatt	gtcaagtatt	tgtgagtacg	atttgctct	actattctcc	ccacacgcta	578
71	tcgttccatt	gcctgcattcc	gatcgccggt	cttgcattat	agttcattgg	gatggcgggt	638
72	ctcaatccat	cgcagcgaag	agagggtcg	agctgtatac	tgtcattgac	ttcgaacgtg	698
73	actataagtc	atggcgattt	gacgccgatc	tatgaacggc	tgaccaatct	agaagcgtct	758
74	acggagttat	tacatcgctc	catttccgat	atattccacta	ctgtctcaaa	tatttctgca	818
75	aatttacaag	acatgaccca	taccttggat	gatgtaactg	ctaatttaga	cgggttgagg	878
76	accactgtta	ctgcacttca	ggattccgtc	tccattctgt	ctacaaatgt	gactgactta	938
77	acgaacacat	cctctgcgca	cgcggcgaca	ctatcttcac	ttcaaactac	ggttgacgga	998
78	aactccactg	ccatctccaa	tttgaagagt	gatgtatcgt	cgaacgggtt	agctattaca	1058
79	gatctgcagg	atcggtttaa	atcattggag	tctaccgcga	gtcatggct	atcttttcg	1118
80	cctccgccta	gtgtcgctga	cggcgtgggt	tcattagaca	tggaccctta	cttctgttct	1178
81	caacgagttt	ctttaacatc	atactcgccg	gaggctcaac	taatgcaatt	tcggtggatg	1238
82	gcacggggta	ctaacggatc	atctgatacc	attgacatga	ccgttaacgc	tcactgtcat	1298
83	ggaagacgca	ctgattatat	gatgtcgatc	acggaaatc	tcacggtcac	tagtaacgtc	1358
84	gtgttattaa	ccttcgattt	aagtgcatac	acgcataatcc	catcagacact	agcacgtctt	1418
85	gttcccagtg	cgggattcca	agctgcgtcg	ttccctgtgg	acgtatcatt	cacccgcgat	1478
86	tctgcgactc	atgcgtacca	agcgtatggg	gtgtactcga	gctcacgtgt	cttcacaatt	1538
87	actttcccaa	ccggaggtga	tggtacagcg	aacattcgat	ccttgaccgt	gcgtaccggc	1598
88	atcgacacct	aagggtgtggc	gccgtactgg	gattggttat	tcatc		1643

90 <210> SEQ ID NO: 2

91 <211> LENGTH: 98

92 <212> TYPE: PRT

93 <213> ORGANISM: avian reovirus strain 176

95 <400> SEQUENCE: 2

96	Met	Leu	Arg	Met	Pro	Pro	Gly	Ser	Cys	Asn	Gly	Ala	Thr	Ala	Val	Phe
97	1			5					10						15	
98	Gly	Asn	Val	His	Cys	Gln	Ala	Ala	Gln	Asn	Thr	Ala	Gly	Gly	Asp	Leu
99							20			25					30	
100	Gln	Ala	Thr	Ser	Ser	Ile	Ile	Ala	Tyr	Trp	Pro	Tyr	Leu	Ala	Ala	Gly
101							35			40					45	
102	Gly	Gly	Phe	Leu	Leu	Ile	Val	Ile	Ile	Phe	Ala	Leu	Leu	Tyr	Cys	Cys
103							50			55					60	
104	Lys	Ala	Lys	Val	Lys	Ala	Asp	Ala	Ala	Arg	Ser	Val	Phe	His	Arg	Glu
105							65			70					75	80
106	Leu	Val	Ala	Leu	Ser	Ser	Gly	Lys	His	Asn	Ala	Met	Ala	Pro	Pro	Tyr
107							85			90					95	

108 Asp Val

110 <210> SEQ ID NO: 3

111 <211> LENGTH: 146

112 <212> TYPE: PRT

113 <213> ORGANISM: avian reovirus strain 176

115 <400> SEQUENCE: 3

116	Met	Gln	Trp	Leu	Arg	His	Thr	Thr	Phe	Glu	Val	Gln	Arg	Phe	Asn	Phe
117	1			5					10						15	
118	Cys	Pro	Leu	Ser	Leu	Arg	Glu	Leu	Ala	Ile	Pro	Ser	Phe	Thr	Ala	Ile
119								20			25				30	
120	Thr	Gly	Ala	Asp	Pro	Ser	Gln	Tyr	Phe	Asn	Ile	Glu	Leu	Pro	His	Thr

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121 35 40 45
 122 His Pro Leu Tyr Ser Lys Leu Pro Thr Leu Leu Ser Gln Pro Cys Arg
 123 50 55 60
 124 Val His Val Arg Leu Ile Arg Arg Phe Ala Leu Tyr Ser Thr Leu Ser
 125 65 70 75 80
 126 Ser Ile Cys Glu Tyr Asp Cys Ala Leu Leu Phe Ser Pro His Ala Ile
 127 85 90 95
 128 Val Pro Leu Pro Ala Ser Asp Arg Arg Ser Cys Leu Ile Val His Trp
 129 100 105 110
 130 Asp Gly Gly Ser Gln Ser Ile Ala Ala Lys Arg Gly Arg Gln Leu Asp
 131 115 120 125
 132 Thr Val Ile Asp Phe Glu Arg Asp Tyr Lys Ser Trp Arg Phe Asp Ala
 133 130 135 140
 134 Asp Leu
 135 145
 137 <210> SEQ ID NO: 4
 138 <211> LENGTH: 326
 139 <212> TYPE: PRT
 140 <213> ORGANISM: avian reovirus strain 176
 142 <400> SEQUENCE: 4
 143 Met Ala Gly Leu Asn Pro Ser Gln Arg Arg Glu Val Val Ser Leu Ile
 144 1 5 10 15
 145 Leu Ser Leu Thr Ser Asn Val Thr Ile Ser His Gly Asp Leu Thr Pro
 146 20 25 30
 147 Ile Tyr Glu Arg Leu Thr Asn Leu Glu Ala Ser Thr Glu Leu Leu His
 148 35 40 45
 149 Arg Ser Ile Ser Asp Ile Ser Thr Thr Val Ser Asn Ile Ser Ala Asn
 150 50 55 60
 151 Leu Gln Asp Met Thr His Thr Leu Asp Asp Val Thr Ala Asn Leu Asp
 152 65 70 75 80
 153 Gly Leu Arg Thr Thr Val Thr Ala Leu Gln Asp Ser Val Ser Ile Leu
 154 85 90 95
 155 Ser Thr Asn Val Thr Asp Leu Thr Asn Thr Ser Ser Ala His Ala Ala
 156 100 105 110
 157 Thr Leu Ser Ser Leu Gln Thr Thr Val Asp Gly Asn Ser Thr Ala Ile
 158 115 120 125
 159 Ser Asn Leu Lys Ser Asp Val Ser Ser Asn Gly Leu Ala Ile Thr Asp
 160 130 135 140
 161 Leu Gln Asp Arg Val Lys Ser Leu Glu Ser Thr Ala Ser His Gly Leu
 162 145 150 155 160
 163 Ser Phe Ser Pro Pro Leu Ser Val Ala Asp Gly Val Val Ser Leu Asp
 164 165 170 175
 165 Met Asp Pro Tyr Phe Cys Ser Gln Arg Val Ser Leu Thr Ser Tyr Ser
 166 180 185 190
 167 Ala Glu Ala Gln Leu Met Gln Phe Arg Trp Met Ala Arg Gly Thr Asn
 168 195 200 205
 169 Gly Ser Ser Asp Thr Ile Asp Met Thr Val Asn Ala His Cys His Gly
 170 210 215 220
 171 Arg Arg Thr Asp Tyr Met Met Ser Ser Thr Gly Asn Leu Thr Val Thr

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172	225	230	235	240
173	Ser Asn Val Val Leu Leu Thr Phe Asp Leu Ser Asp Ile Thr His Ile			
174	245	250	255	
175	Pro Ser Asp Leu Ala Arg Leu Val Pro Ser Ala Gly Phe Gln Ala Ala			
176	260	265	270	
177	Ser Phe Pro Val Asp Val Ser Phe Thr Arg Asp Ser Ala Thr His Ala			
178	275	280	285	
179	Tyr Gln Ala Tyr Gly Val Tyr Ser Ser Ser Arg Val Phe Thr Ile Thr			
180	290	295	300	
181	Phe Pro Thr Gly Gly Asp Gly Thr Ala Asn Ile Arg Ser Leu Thr Val			
182	305	310	315	320
183	Arg Thr Gly Ile Asp Thr			
184	325			
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187	<211> LENGTH: 1643			
188	<212> TYPE: DNA			
189	<213> ORGANISM: avian reovirus strain 138			
191	<220> FEATURE:			
192	<221> NAME/KEY: CDS			
193	<222> LOCATION: (25)...(318)			
194	<223> OTHER INFORMATION: nucleotide sequence encoding P11 protein (SEQ ID NO:6)			
196	<220> FEATURE:			
197	<221> NAME/KEY: misc_feature			
198	<222> LOCATION: (293)...(730)			
199	<223> OTHER INFORMATION: CDS encoding P16 protein (SEQ ID NO:7)			
201	<220> FEATURE:			
202	<221> NAME/KEY: misc_feature			
203	<222> LOCATION: (630)...(1607)			
204	<223> OTHER INFORMATION: CDS encoding sigma3 protein (SEQ ID NO:8)			
206	<400> SEQUENCE: 5			
207	gcttttcaa tcccttgttt gtcg atg ctg cgt atg cct ccc ggt tcg tgt			51
208	Met Leu Arg Met Pro Pro Gly Ser Cys			
209	1 5			
211	aac ggt gca aca gct atc ttt ggt aac gtc cat tgt cag gcg gct caa			99
212	Asn Gly Ala Thr Ala Ile Phe Gly Asn Val His Cys Gln Ala Ala Gln			
213	10 15 20 25			
215	aat act gcc ggc ggc gac ttg caa gct acc tca tcc ata att gcc tat			147
216	Asn Thr Ala Gly Gly Asp Leu Gln Ala Thr Ser Ser Ile Ile Ala Tyr			
217	30 35 40			
219	tgg cct tat cta gcg gcg ggt ggt ttt ttg ttg att att att att			195
220	Trp Pro Tyr Leu Ala Ala Gly Gly Phe Leu Leu Ile Ile Ile Ile			
221	45 50 55			
223	ttt gcc atc ttc tac tgt tgt aag gct aaa gtt aaa gcg gac gct gca			243
224	Phe Ala Ile Phe Tyr Cys Cys Lys Ala Lys Val Lys Ala Asp Ala Ala			
225	60 65 70			
227	cgg agt gtt ttc cac cgt gag ctt gta gca ctg agc tct ggt aag cac			291
228	Arg Ser Val Phe His Arg Glu Leu Val Ala Leu Ser Ser Gly Lys His			
229	75 80 85			
231	aat gca atg gct ccg cca tac gac gtt tgaagtgc当地 cgctttgatt			338

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232 Asn Ala Met Ala Pro Pro Tyr Asp Val
233 90 95 398
235 tctgccaaat atcacttcgt gagcttgcca cccatcggt tactgctata attgggattg 458
236 acccatcactt ttatTTaaat attgagctt cgcacacgca tcctctac tctaagttgc 518
237 cgactctgtt atcgcagccc tgccgagtt acgtgcgtt gattcgtaga ttgcgtct 578
238 gttcaacgct gtcgagttatc tgcgagttacg attgtgcgtt actacttcc ccacacgcca 638
239 tcactccact gtcctcatcc gatcagcgat cttatcttat agttcattgg gatggcgggt 698
240 ctcacatccat cacagcgaag agaggtcgatc agcttgatac tgcatttgac ttcaacgcg 758
241 catataaaatc atggcgattt gacgccaatc tatgaacggg tgaccagtt agaagcgct 818
242 gcggaatcac tatatcgctc catttccagc atgtctacta ccgtttcaga catttcagca 878
243 gatttgcaga acgtgactcg cgccttgat gatgtgactg ctaattttaga tggtatgaga 938
244 gtcaccattt ctagcttca agattctgtg tccactctt caacgactgt aactgattta 998
245 acaaacacct cttctgtca ctcggaaagca ctgtcttac tccgaactat agttgatggg 1058
246 aactccacta ccattgataa ttgaaaatg gatgtatcat caaacggct tgctatcaca 1118
247 gacctgcaga gtcgtgttaa atccttgaa tctgtttcga gtcacggct atcttttcg 1178
248 cttcccttta gtgtcgctga cgacgtatg tcgttgatg tggaccctta cttttgtct 1238
249 cagcgagtc ctttgacatc atactcagca gaagctcaac tgatgcaatt ccaatggatg 1298
250 gcaagaggtg ctaacggatc atcagacact attgacatga ccgtcaatgc tcactgtcat 1358
251 gggagacgca ctgatttacat aatgtcgatcc acgggagggtc ttacagttac tagtaatgcc 1418
252 gtgtctttaa ctttcgactt gagttacatt acacgcctcc caccagacct ctcgcgtctt 1478
253 gttcccaatg caggattcca agccgcgtcg ttcccccgtgg atgtatccctt caccagagat 1538
254 tcgacaactc atacatatca agcttatgga gtgtattcta gttcgctgtt attaccatc 1598
255 actttcccgaa ctgggtgtga cggcccgca aatatccgtt tcctaaccgt gcttaccggc 1643
256 atcgacacactt aagggtgtggc gccgtacggg gattggttat tcata
258 <210> SEQ ID NO: 6
259 <211> LENGTH: 98
260 <212> TYPE: PRT
261 <213> ORGANISM: avian reovirus strain 138
263 <400> SEQUENCE: 6
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265 1 5 10 15
266 Gly Asn Val His Cys Gln Ala Ala Gln Asn Thr Ala Gly Gly Asp Leu
267 20 25 30
268 Gln Ala Thr Ser Ser Ile Ile Ala Tyr Trp Pro Tyr Leu Ala Ala Gly
269 35 40 45
270 Gly Gly Phe Leu Leu Ile Ile Ile Phe Ala Ile Phe Tyr Cys Cys
271 50 55 60
272 Lys Ala Lys Val Lys Ala Asp Ala Ala Arg Ser Val Phe His Arg Glu
273 65 70 75 80
274 Leu Val Ala Leu Ser Ser Gly Lys His Asn Ala Met Ala Pro Pro Tyr
275 85 90 95
276 Asp Val
278 <210> SEQ ID NO: 7
279 <211> LENGTH: 146
280 <212> TYPE: PRT
281 <213> ORGANISM: avian reovirus strain 138
283 <400> SEQUENCE: 7
284 Met Gln Trp Leu Arg His Thr Thr Phe Glu Val Gln Arg Phe Asp Phe
285 1 5 10 15

VERIFICATION SUMMARY
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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date